



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/468,002

DATE: 03/31/2003

TIME: 16:26:36

Input Set : N:\Crf3\RULE60\09468002.raw

Output Set: N:\CRF4\03312003\I468002.raw

ENTERED

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1 <110> APPLICANT: Negulescu, Paul
2   Offermanns, Stefan
3   Simon, Melvin
4   Zuker, Charles
5 <120> TITLE OF INVENTION: PROMISCUOUS G-PROTEINS COMPOSITIONS AND THEIR USE
6 <130> FILE REFERENCE: 08366/002001
7 <140> CURRENT APPLICATION NUMBER: 09/468,002
8 <141> CURRENT FILING DATE: 1999-12-20
9 <150> PRIOR APPLICATION NUMBER: US/08/878,801
10 <151> PRIOR FILING DATE: 1997-06-19
11 <150> PRIOR APPLICATION NUMBER: US 60/020,234
12 <151> PRIOR FILING DATE: 1996-06-21
13 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: FastSEQ for Windows Version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1125
18 <212> TYPE: DNA
19 <213> ORGANISM: Mus musculus
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (1)...(1122)
23 <400> SEQUENCE: 1
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25   Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
26       1             5             10             15
27   gat gag aag gcc gcc cgc gtc gac cag gag atc aac agg atc ctc      96
28   Asp Glu Lys Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
29       20             25             30
30   ttg gag cag aag aag cag gac cgc ggg gag ctg aag ctg ctg ctt ttg    144
31   Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu Leu
32       35             40             45
33   ggc cca ggc gag agc ggg aag agc acc ttc atc aag cag atg cgg atc    192
34   Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
35       50             55             60
36   atc cac ggc gcc gcc tac tgc gag gag gag cgc aag ggc ttc cgg ccc    240
37   Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
38       65             70             75             80
39   ctg gtc tac cag aac atc ttc gtc tcc atg cgg gcc atg atc gag gcc    288
40   Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
41       85             90             95
42   atg gag cgg ctg cag att cca ttc agc agg ccc gag agc aag cac cac    336
43   Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
44       100            105            110

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45	gct agc ctg gtc atg agc cag gac ccc tat aaa gtg acc acg ttt gag	384
46	Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu	
47	115 120 125	
48	aag cgc tac gct gcg gcc atg cag tgg ctg tgg agg gat gcc ggc atc	432
49	Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile	
50	130 135 140	
51	cgg gcc tgc tat gag cgt cgg cgg gaa ttc cac ctg ctc gat tca gcc	480
52	Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala	
53	145 150 155 160	
54	gtg tac tac ctg tcc cac ctg gag cgc atc acc gag gag ggc tac gtc	528
55	Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val	
56	165 170 175	
57	ccc aca gct cag gac gtg ctc cgc agc cgc atg ccc acc act ggc atc	576
58	Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile	
59	180 185 190	
60	aac gag tac tgc ttc tcc gtg cag aaa acc aac ctg cgg atc gtg gac	624
61	Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp	
62	195 200 205	
63	gtc ggg ggc cag aag tca gag cgt aag aaa tgg atc cat tgt ttc gag	672
64	Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu	
65	210 215 220	
66	aac gtg atc gcc ctc atc tac ctg gcc tca ctg agt gaa tac gac cag	720
67	Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln	
68	225 230 235 240	
69	tgc ctg gag gag aac aac cag gag aac cgc atg aag gag agc ctc gca	768
70	Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala	
71	245 250 255	
72	ttg ttt ggg act atc ctg gaa cta ccc tgg ttc aaa agc aca tcc gtc	816
73	Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val	
74	260 265 270	
75	atc ctc ttt ctc aac aaa acc gac atc ctg gag gag aaa atc ccc acc	864
76	Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr	
77	275 280 285	
78	tcc cac ctg gct acc tat ttc ccc agt ttc cag ggc cct aag cag gat	912
79	Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp	
80	290 295 300	
81	gct gag gca gcc aag agg ttc atc ctg gac atg tac acg agg atg tac	960
82	Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr	
83	305 310 315 320	
84	acc ggg tgc gtg gac ggc ccc gag ggc agc aag aag ggc gca cga tcc	1008
85	Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser	
86	325 330 335	
87	cga cgc ctt ttc agc cac tac aca tgt gcc aca gac aca cag aac atc	1056
88	Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile	
89	340 345 350	
90	cgc aag gtc ttc aag gac gtg cgg gac tgc gtg ctc gcc cgc tac ctg	1104
91	Arg Lys Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu	
92	355 360 365	
93	gac gag atc aac ctg ctg tga	1125

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94      Asp Glu Ile Asn Leu Leu
95      370
97 <210> SEQ ID NO: 2
98 <211> LENGTH: 374
99 <212> TYPE: PRT
100 <213> ORGANISM: Mus musculus
101 <400> SEQUENCE: 2
102      Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
103      1          5          10          15
104      Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
105      20          25          30
106      Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu
107      35          40          45
108      Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
109      50          55          60
110      Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
111      65          70          75          80
112      Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
113      85          90          95
114      Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
115      100          105          110
116      Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
117      115          120          125
118      Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile
119      130          135          140
120      Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
121      145          150          155          160
122      Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val
123      165          170          175
124      Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
125      180          185          190
126      Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
127      195          200          205
128      Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
129      210          215          220
130      Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
131      225          230          235          240
132      Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
133      245          250          255
134      Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
135      260          265          270
136      Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
137      275          280          285
138      Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
139      290          295          300
140      Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
141      305          310          315          320
142      Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser
143      325          330          335

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144   Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile
145           340                               345                 350
146   Arg Lys Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
147           355                               360                 365
148   Asp Glu Ile Asn Leu Leu
149           370
151 <210> SEQ ID NO: 3
152 <211> LENGTH: 1125
153 <212> TYPE: DNA
154 <213> ORGANISM: Homo sapiens
155 <220> FEATURE:
156 <221> NAME/KEY: CDS
157 <222> LOCATION: (1)...(1122)
158 <400> SEQUENCE: 3
159   atg gcc cgg tcc ctg act tgg ggc tgc tgt ccc tgg tgc ctg aca gag      48
160   Met Ala Arg Ser Leu Thr Trp Gly Cys Cys Pro Trp Cys Leu Thr Glu
161       1               5               10               15
162   gag gag aag act gcc gcc aga atc gac cag gag atc aac agg att ttg      96
163   Glu Glu Lys Thr Ala Ala Arg Ile Asp Gln Glu Ile Asn Arg Ile Leu
164           20               25               30
165   ttg gaa cag aaa aaa caa gag cgc gag gaa ttg aaa ctc ctg ctg ttg      144
166   Leu Glu Gln Lys Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu
167           35               40               45
168   ggg cct ggt gag agc ggg aag agt acg ttc atc aag cag atg cgc atc      192
169   Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
170           50               55               60
171   att cac ggt gtg ggc tac tgc gag gag gac cgc aga gcc ttc cgg ctg      240
172   Ile His Gly Val Gly Tyr Ser Glu Glu Asp Arg Arg Ala Phe Arg Leu
173       65               70               75               80
174   ctc atc tac cag aac atc ttc gtc tcc atg cag gcc atg ata gat gcg      288
175   Leu Ile Tyr Gln Asn Ile Phe Val Ser Met Gln Ala Met Ile Asp Ala
176           85               90               95
177   atg gac cgg ctg cag atc ccc ttc agc agg cct gac agc aag cag cac      336
178   Met Asp Arg Leu Gln Ile Pro Phe Ser Arg Pro Asp Ser Lys Gln His
179           100              105              110
180   gcc agc cta gtg atg acc cag gac ccc tat aaa gtg agc aca ttc gag      384
181   Ala Ser Leu Val Met Thr Gln Asp Pro Tyr Lys Val Ser Thr Phe Glu
182           115              120              125
183   aag cca tat gca gtg gcc atg cag tac ctg tgg cgg gac gcg ggc atc      432
184   Lys Pro Tyr Ala Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile
185           130              135              140
186   cgt gca tgc tac gag cga agg cgt gaa ttc cac ctt ctg gac tcc gcg      480
187   Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
188       145              150              155              160
189   gtg tat tac ctg tca cac ctg gag cgc ata gag gac agc tac atc      528
190   Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile
191           165              170              175
192   ccc act gcg caa gac gtg ctg cgc agt cgc atg ccc acc aca ggc atc      576
193   Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile

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194		180		185		190		
195	aat gag tac tgc ttc tcc gtg aag aaa acc aaa ctg cgc atc gtg gat							624
196	Asn Glu Tyr Cys Phe Ser Val Lys Lys Thr Lys Leu Arg Ile Val Asp							
197		195		200		205		
198	gtt ggt ggc cag agg tca gag cgt agg aaa tgg att cac tgt ttc gag							672
199	Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu							
200		210		215		220		
201	aac gtg att gcc ctc atc tac ctg gcc tcc ctg agc gag tat gac cag							720
202	Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln							
203		225		230		235		240
204	tgc cta gag gag aac gat cag gag aac cgc atg gag gag agt ctc gct							768
205	Cys Leu Glu Glu Asn Asp Gln Glu Asn Arg Met Glu Glu Ser Leu Ala							
206		245		250		255		
207	ctg ttc agc acg atc cta gag ctg ccc tgg ttc aag agc acc tcg gtc							816
208	Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val							
209		260		265		270		
210	atc ctc ttc ctc aac aag acg gac atc ctg gaa gat aag att cac acc							864
211	Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr							
212		275		280		285		
213	tcc cac ctg gcc aca tac ttc ccc agc ttc cag gga ccc cgg cga gac							912
214	Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp							
215		290		295		300		
216	gca gag gcc gcc aag agc ttc atc ttg gac atg tat gcg cgc gtg tac							960
217	Ala Glu Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr							
218		305		310		315		320
219	gcg agc tgc gca gag ccc cag gac ggt ggc agg aaa ggc tcc cgc gcg							1008
220	Ala Ser Cys Ala Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala							
221		325		330		335		
222	cgc cgc ttc ttc gca cac ttc acc tgt gcc acg gac acg caa agc gtc							1056
223	Arg Arg Phe Phe Ala His Phe Thr Cys Ala Thr Asp Thr Gln Ser Val							
224		340		345		350		
225	cgc agc gtg ttc aag gac gtg cgg gac tcg gtg ctg gcc cgg tac ctg							1104
226	Arg Ser Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu							
227		355		360		365		
228	gac gag atc aac ctg ctg tga							1125
229	Asp Glu Ile Asn Leu Leu							
230		370						
232	<210> SEQ ID NO: 4							
233	<211> LENGTH: 374							
234	<212> TYPE: PRT							
235	<213> ORGANISM: Homo sapiens							
236	<400> SEQUENCE: 4							
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238	1 5 10 15							
239	Glu Glu Lys Thr Ala Ala Arg Ile Asp Gln Glu Ile Asn Arg Ile Leu							
240	20 25 30							
241	Leu Glu Gln Lys Lys Gln Glu Arg Glu Glu Leu Lys Leu Leu Leu Leu							
242	35 40 45							
243	Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile							

VERIFICATION SUMMARY

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